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RAW SEQUENCE LISTING   DATE: 02/20/2004
PATENT APPLICATION: **US/10/645,012**   TIME: 14:42:41

Input Set : **N:\Crf3\RULE60\10645012.RAW.txt**
Output Set: **N:\CRF4\02202004\J645012.raw**

```
 1 <110> APPLICANT: Tsuchiya, Masayuki
 2         Saito, Mikiyoshi
 3         Ohtomo, Toshihiko
 4 <120> TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING
 5 <130> FILE REFERENCE: 06501-070001
 6 <140> CURRENT APPLICATION NUMBER: 10/645,012
 7 <141> CURRENT FILING DATE: 2003-08-21
 8 <150> PRIOR APPLICATION NUMBER: US/09/700,820
 9 <151> PRIOR FILING DATE: 2000-11-20
10 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02341
11 <151> PRIOR FILING DATE: 1999-04-30
12 <150> PRIOR APPLICATION NUMBER: JP 10/138652
13 <151> PRIOR FILING DATE: 1998-05-20
14 <150> PRIOR APPLICATION NUMBER: JP 10/279876
15 <151> PRIOR FILING DATE: 1998-10-01
16 <160> NUMBER OF SEQ ID NOS: 39
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 15
20 <212> TYPE: PRT
21 <213> ORGANISM: Artificial Sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: Description of Artificial Sequence:Peptide Linker Sequence
24 <400> SEQUENCE: 1
25       Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
26        1               5                   10                  15
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 1035
30 <212> TYPE: DNA
31 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1035)
35 <400> SEQUENCE: 2
36       atg ctg gcc gtc ggc tgc gcg ctg ctg gct gcc ctg ctg gcc gcg ccg      48
37       Met Leu Ala Val Gly Cys Ala Leu Leu Ala Ala Leu Leu Ala Ala Pro
38        1               5                   10                  15
39       gga gcg gcg ctg gcc cca agg cgc tgc cct gcg cag gag gtg gca aga      96
40       Gly Ala Ala Leu Ala Pro Arg Arg Cys Pro Ala Gln Glu Val Ala Arg
41                       20                  25                  30
42       ggc gtg ctg acc agt ctg cca gga gac agc gtg act ctg acc tgc ccg     144
43       Gly Val Leu Thr Ser Leu Pro Gly Asp Ser Val Thr Leu Thr Cys Pro
44                    35                  40                  45
45       ggg gta gag ccg gaa gac aat gcc act gtt cac tgg gtg ctc agg aag     192
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46      Gly Val Glu Pro Glu Asp Asn Ala Thr Val His Trp Val Leu Arg Lys
47           50              55              60
48      ccg gct gca ggc tcc cac ccc agc aga tgg gct ggc atg gga agg agg    240
49      Pro Ala Ala Gly Ser His Pro Ser Arg Trp Ala Gly Met Gly Arg Arg
50      65              70              75              80
51      ctg ctg ctg agg tcg gtg cag ctc cac gac tct gga aac tat tca tgc    288
52      Leu Leu Leu Arg Ser Val Gln Leu His Asp Ser Gly Asn Tyr Ser Cys
53                      85              90              95
54      tac cgg gcc ggc cgc cca gct ggg act gtg cac ttg ctg gtg gat gtt    336
55      Tyr Arg Ala Gly Arg Pro Ala Gly Thr Val His Leu Leu Val Asp Val
56                  100             105             110
57      ccc ccc gag gag ccc cag ctc tcc tgc ttc cgg aag agc ccc ctc agc    384
58      Pro Pro Glu Glu Pro Gln Leu Ser Cys Phe Arg Lys Ser Pro Leu Ser
59              115             120             125
60      aat gtt gtt tgt gag tgg ggt cct cgg agc acc cca tcc ctg acg aca    432
61      Asn Val Val Cys Glu Trp Gly Pro Arg Ser Thr Pro Ser Leu Thr Thr
62              130             135             140
63      aag gct gtg ctc ttg gtg agg aag ttt cag aac agt ccg gcc gaa gac    480
64      Lys Ala Val Leu Leu Val Arg Lys Phe Gln Asn Ser Pro Ala Glu Asp
65      145             150             155             160
66      ttc cag gag ccg tgc cag tat tcc cag gag tcc cag aag ttc tcc tgc    528
67      Phe Gln Glu Pro Cys Gln Tyr Ser Gln Glu Ser Gln Lys Phe Ser Cys
68                      165             170             175
69      cag tta gca gtc ccg gag gga gac agc tct ttc tac ata gtg tcc atg    576
70      Gln Leu Ala Val Pro Glu Gly Asp Ser Ser Phe Tyr Ile Val Ser Met
71                  180             185             190
72      tgc gtc gcc agt agt gtc ggg agc aag ttc agc aaa act caa acc ttt    624
73      Cys Val Ala Ser Ser Val Gly Ser Lys Phe Ser Lys Thr Gln Thr Phe
74                  195             200             205
75      cag ggt tgt gga atc ttg cag cct gat ccg cct gcc aac atc aca gtc    672
76      Gln Gly Cys Gly Ile Leu Gln Pro Asp Pro Pro Ala Asn Ile Thr Val
77              210             215             220
78      act gcc gtg gcc aga aac ccc cgc tgg ctc agt gtc acc tgg caa gac    720
79      Thr Ala Val Ala Arg Asn Pro Arg Trp Leu Ser Val Thr Trp Gln Asp
80      225             230             235             240
81      ccc cac tcc tgg aac tca tct ttc tac aga cta cgg ttt gag ctc aga    768
82      Pro His Ser Trp Asn Ser Ser Phe Tyr Arg Leu Arg Phe Glu Leu Arg
83                      245             250             255
84      tat cgg gct gaa cgg tca aag aca ttc aca aca tgg atg gtc aag gac    816
85      Tyr Arg Ala Glu Arg Ser Lys Thr Phe Thr Thr Trp Met Val Lys Asp
86                  260             265             270
87      ctc cag cat cac tgt gtc atc cac gac gcc tgg agc ggc ctg agg cac    864
88      Leu Gln His His Cys Val Ile His Asp Ala Trp Ser Gly Leu Arg His
89                  275             280             285
90      gtg gtg cag ctt cgt gcc cag gag gag ttc ggg caa ggc gag tgg agc    912
91      Val Val Gln Leu Arg Ala Gln Glu Glu Phe Gly Gln Gly Glu Trp Ser
92              290             295             300
93      gag tgg agc ccg gag gcc atg ggc acg cct tgg aca gaa tcc agg agt    960
94      Glu Trp Ser Pro Glu Ala Met Gly Thr Pro Trp Thr Glu Ser Arg Ser
```

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 95          305                    310                    315                    320
 96     cct cca gct gag aac gag gtg tcc acc ccc atg cag gca ctt act act          1008
 97     Pro Pro Ala Glu Asn Glu Val Ser Thr Pro Met Gln Ala Leu Thr Thr
 98                            325                    330                    335
 99     aat aaa gac gat gat aat att ctc ttc                                      1035
100      Asn Lys Asp Asp Asp Asn Ile Leu Phe
101                            340                    345
103 <210> SEQ ID NO: 3
104 <211> LENGTH: 40
105 <212> TYPE: DNA
106 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Description of Artificial Sequence: "IL6R1", an artificially
synthesized primer sequence
109 <400> SEQUENCE: 3
110      ttcgaattcc caccatgctg gccgtcggct gcgcgctgct                               40
112 <210> SEQ ID NO: 4
113 <211> LENGTH: 36
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
117 <223> OTHER INFORMATION: Description of Artificial Sequence: "IL6R2", an artificially
synthesized primer sequence
118 <400> SEQUENCE: 4
119      ttcgaattcg aagagaatat tatcatcgtc tttatt                                   36
121 <210> SEQ ID NO: 5
122 <211> LENGTH: 768
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <221> NAME/KEY: CDS
127 <222> LOCATION: (1)..(768)
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Description of Artificial Sequence: a designed single chain
Fv gene sequence
130 <400> SEQUENCE: 5
131      cag gtc caa ctg cag gag agc ggt cca ggt ctt gtg aga cct agc cag           48
132      Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
133      1               5                    10                     15
134      acc ctg agc ctg acc tgc acc gtg tct ggc tac tca att acc agc gat           96
135      Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
136                      20                     25                     30
137      cat gcc tgg agc tgg gtt cgc cag cca cct gga cga ggt ctt gag tgg          144
138      His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
139                      35                     40                     45
140      att gga tac att agt tat agt gga atc aca acc tat aat cca tct ctc          192
141      Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu
142                      50                     55                     60
143      aaa tcc aga gtg aca atg ctg aga gac acc agc aag aac cag ttc agc          240
144      Lys Ser Arg Val Thr Met Leu Arg Asp Thr Ser Lys Asn Gln Phe Ser
145      65                      70                     75                     80
146      ctg aga ctc agc agc gtg aca gcc gcc gac acc gcg gtt tat tat tgt          288
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```
147      Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
148                       85                  90                  95
149      gca aga tcc cta gct cgg act acg gct atg gac tac tgg ggt caa ggc      336
150      Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly
151                      100                 105                 110
152      agc ctc gtc aca gtc tcc tca ggt ggt ggt ggt tcg ggt ggt ggt ggt      384
153      Ser Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
154                      115                 120                 125
155      tcg ggt ggt ggc gga tcg gac atc cag atg acc cag agc cca agc agc      432
156      Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
157                      130                 135                 140
158      ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aga gcc agc      480
159      Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
160      145                 150                 155                 160
161      cag gac atc agc agt tac ctg aat tgg tac cag cag aag cca gga aag      528
162      Gln Asp Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
163                      165                 170                 175
164      gct cca aag ctg ctg atc tac tac acc tcc aga ctg cac tct ggt gtg      576
165      Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His Ser Gly Val
166                      180                 185                 190
167      cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc      624
168      Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr
169                      195                 200                 205
170      atc agc agc ctc cag cca gag gac atc gct acc tac tac tgc caa cag      672
171      Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln
172                      210                 215                 220
173      ggt aac acg ctt cca tac acg ttc ggc caa ggg acc aag gtg gaa atc      720
174      Gly Asn Thr Leu Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
175      225                 230                 235                 240
176      aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat      768
177      Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
178                      245                 250                 255
180 <210> SEQ ID NO: 6
181 <211> LENGTH: 32
182 <212> TYPE: DNA
183 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence: "TMT1", an artificially
synthesized primer sequence
186 <400> SEQUENCE: 6
187      ggtgtcgact cccaggtcca actgcaggag ag                                  32
189 <210> SEQ ID NO: 7
190 <211> LENGTH: 32
191 <212> TYPE: DNA
192 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK1", an artificially
synthesized primer sequence
195 <400> SEQUENCE: 7
196      ctcgtcacag tctcctcagg tggtggtggt tc                                  32
198 <210> SEQ ID NO: 8
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199 <211> LENGTH: 38
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK3", an artificially
synthesized primer sequence
204 <400> SEQUENCE: 8
205      gacatccaga tgacccagag cccaagcagc ctgagcgc                    38
207 <210> SEQ ID NO: 9
208 <211> LENGTH: 63
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Description of Artificial Sequence: "SCP-C", an artificially
synthesized primer sequence
213 <400> SEQUENCE: 9
214      gctgaattct tattatttat cgtcatcgtc tttgtagtca agcttatcag atggcgggaa    60
215      gat                                                          63
217 <210> SEQ ID NO: 10
218 <211> LENGTH: 9
219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial Sequence
221 <220> FEATURE:
222 <223> OTHER INFORMATION: Description of Artificial Sequence: FLAG peptide
223 <400> SEQUENCE: 10
224      Met Asp Tyr Lys Asp Asp Asp Asp Lys
225        1               5
227 <210> SEQ ID NO: 11
228 <211> LENGTH: 34
229 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK2", an artificially
synthesized primer sequence
233 <400> SEQUENCE: 11
234      aaccaccacc acctgaggag actgtgacga ggct                        34
236 <210> SEQ ID NO: 12
237 <211> LENGTH: 35
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Artificial Sequence: "LINK4", an artificially
synthesized primer sequence
242 <400> SEQUENCE: 12
243      aggctgcttg ggctctgggt catctggatg tccga                       35
245 <210> SEQ ID NO: 13
246 <211> LENGTH: 36
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence: "TMT2", an artificially
synthesized primer sequence
251 <400> SEQUENCE: 13
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252   atccgcggcc gcttattatt tatcgtcatc gtcttt   36

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/20/2004
PATENT APPLICATION: **US/10/645,012**   TIME: 14:42:42

Input Set : **N:\Crf3\RULE60\10645012.RAW.txt**
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Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 23
Seq#:3; Line(s) 108
Seq#:4; Line(s) 117
Seq#:5; Line(s) 129
Seq#:6; Line(s) 185
Seq#:7; Line(s) 194
Seq#:8; Line(s) 203
Seq#:9; Line(s) 212
Seq#:11; Line(s) 232
Seq#:12; Line(s) 241
Seq#:13; Line(s) 250
Seq#:15; Line(s) 270
Seq#:16; Line(s) 280
Seq#:18; Line(s) 477
Seq#:19; Line(s) 486
Seq#:20; Line(s) 495
Seq#:21; Line(s) 507
Seq#:22; Line(s) 620
Seq#:23; Line(s) 633
Seq#:26; Line(s) 758
Seq#:27; Line(s) 838
Seq#:28; Line(s) 918
Seq#:29; Line(s) 927
Seq#:30; Line(s) 940
Seq#:31; Line(s) 1047
Seq#:32; Line(s) 1056
Seq#:33; Line(s) 1065
Seq#:34; Line(s) 1077
Seq#:35; Line(s) 1205
Seq#:36; Line(s) 1214
Seq#:37; Line(s) 1224
Seq#:38; Line(s) 1233
Seq#:39; Line(s) 1245

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/645,012**

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L:295 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 17, CDS LOCATION:29..2839